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Identification of the rare deep-dwelling goby *Suruga fundicola* Jordan & Snyder, 1901 (Gobiiformes, Gobiidae) from the Yellow Sea

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Abstract

During the 2022 R/V cruises in the Yellow Sea, four goby specimens (51.2–63.5 mm) were captured by using an Agassiz trawl at a water depth of about 70 meters. These specimens were identified as *Suruga fundicola*, mainly by the morphometric characters. Their identification was further confirmed by a molecular phylogenetic analysis based on *12S* and *COI* mtDNA genes. Considering that the four specimens were in good condition and that the original description is brief, a detailed description of the specimens is given. Moreover, the present study presents a preliminary analysis of its phylogenetic position within the *Acanthogobius*-lineage (Gobiidae). The discovery of this goby in the Yellow Sea enriches our knowledge of the fish diversity and distribution of this region, and sheds some light on the ecological habitat of these gobies.

Key Words

Acanthogobius-lineage, distribution, morphology, mtDNA genes, species identification, taxonomy

Introduction

The gobies (order Gobiiformes) include about 2400 species divided into about 320 genera, which are widely distributed throughout the tropical, subtropical, and temperate regions of the world (Parenti 2021; Fricke et al. 2023). These goby species are known from the deep see waters (at a depth of over 300 meters) to elevated mountain streams (at an altitude of over 1000 meters) (Iwata et al. 2000; Shibukawa and Aonuma 2007; Parenti 2021). About 90% of them dwell in marine water, and generally live at the bottom of the sea with a depth of no more than 30 m (Wu and Zhong 2008; Akihito et al. 2013). Only a few species of goby inhabit deep waters; examples from the Western Pacific are species of the genera *Obliquogobius* Koumans, 1941 and *Suruga* Jordan & Snyder, 1901 (Shibukawa and Aonuma 2007; Fujiwara and Shibukawa 2022). According to the record, *Suruga fundicola* Jordan & Snyder, 1901 can inhabit the bottom of deep water off the coast (depth about 40–400 meters; Akihito et al 2013; Choi and Lee 2019).

The goby genus *Suruga* Jordan & Snyder, 1901 of the family Gobiidae comprises only one species, *Suruga fundicola* Jordan & Snyder, 1901 (Akihito et al 2013; Fricke et al. 2023). Based on axial skeletal features, *Suruga* was placed in the *Acanthogobius*-group (sometimes denoted as the tribe Acanthogobiini Parenti 2021) with 7 other genera, *Acanthogobius* Gill, 1859, *Amblychaeturichthys* Bleeker, 1853, *Chaeturichthys* Richardson 1844, *Lophiogobius* Günther, 1873, *Pterogobius* Gill, 1863, *Sagamia* Jordan & Snyder, 1901 and *Siphonogobius* Shibukawa & Iwata, 1998 (Birdsong et al. 1988; Shibukawa 1997).

These eight genera including 18 species, are defined by a unique pattern of the dorsal-pterygiophore formula 3/ I II II I I I 0 (indicating the relationship between the pterygiophores of the dorsal fins and the corresponding spines of the vertebrae), and these genera are regarded as a putative monophyletic assemblage (Akihito et al. 1984; Shibukawa and Iwata 2013a). Mainly based on molecular evidence, the monophyly was only partially confirmed based on few species sequences of this group, and the assemblage was confirmed to be part of the *Acanthogobius*-lineage (a monophyletic lineage of the family Gobiidae comprises about 29 genera) (Agorreta et al. 2013; Thacker and Dawn 2013). The phylogenetic position of *S. fundicola* remained unknown up until now, for the sequence from *S. fundicola* was not included in these molecular studies.

Since its original description, *S. fundicola* has occasionally been found in marine surveys (Kuroda 1957; Yamamuta et al. 1993; Shinohara et al. 2001; Shinohara et al. 2005; Iwatsuki et al. 2017; Choi and Lee 2019; Sonoyama et al. 2020). So far, *S. fundicola* is mainly known from temperate regions of Japan, including off the Pacific coast from Matsushima Bay to Tosa Bay (Fig. 1, black arrows 2 and 3), Japan Sea coast from Aomori Prefecture to Yamaguchi Prefecture (Fig. 1, black arrows 4 and 5), and the Okinawa Trough (black full circle 6) (Akihito et al. 2013). This species is also reported off Tongyeong, South Korea (Fig. 1 blue full circle 7) (Choi and Lee 2019). Although Okiyama (2014) recorded juveniles as *S. fundicola* from two stations of the East China Sea in 1956 (Fig. 1, orange full circle 8 and 9), this species identification was not accepted by subsequent authors (Akihito et al 1984; Wu and Zhong 2008; Akihito et al 2013; Wu and Zhong 2021). So far, there is no record of this species from the Yellow Sea. According to the historical records, there are about 50 goby species known to occur in the Yellow Sea, all of which live in shallow coastal waters (Wu and Zhong 2008; Liu et al. 2015; Parenti 2021).

Two R/V cruises, conducted during 2022, yielded four goby specimens from stations H27 (35°59.69'N, 123°07.63'E) and H12 (33°59.55'N, 123°22.99'E) in the Yellow Sea (see Fig. 1, green triangles). These specimens have notably large eyes, and combined with other morphometric characters these four gobies would conform to *Suruga fundicola* Jordan & Snyder, 1901. But there were a few inconsistent descriptive features, which hampered a definite identification. In order to confirm this morphology-based species identification, *COI* and *12S* genes of mitochondrial DNA of these four specimens were amplified. Phylogenetic analyses of the obtained sequences and the literature available sequences of other *Acanthogobius*-lineage gobies (also including one GenBank-retrieved *12S* sequence of *S. fundicola* from Jogashima Island, Japan, accession number LC069781), showed that the specimens belong to the species *S. fundicola*.

This is the first report on the occurrence of *S. fundicola* in the Yellow Sea based on available specimens.

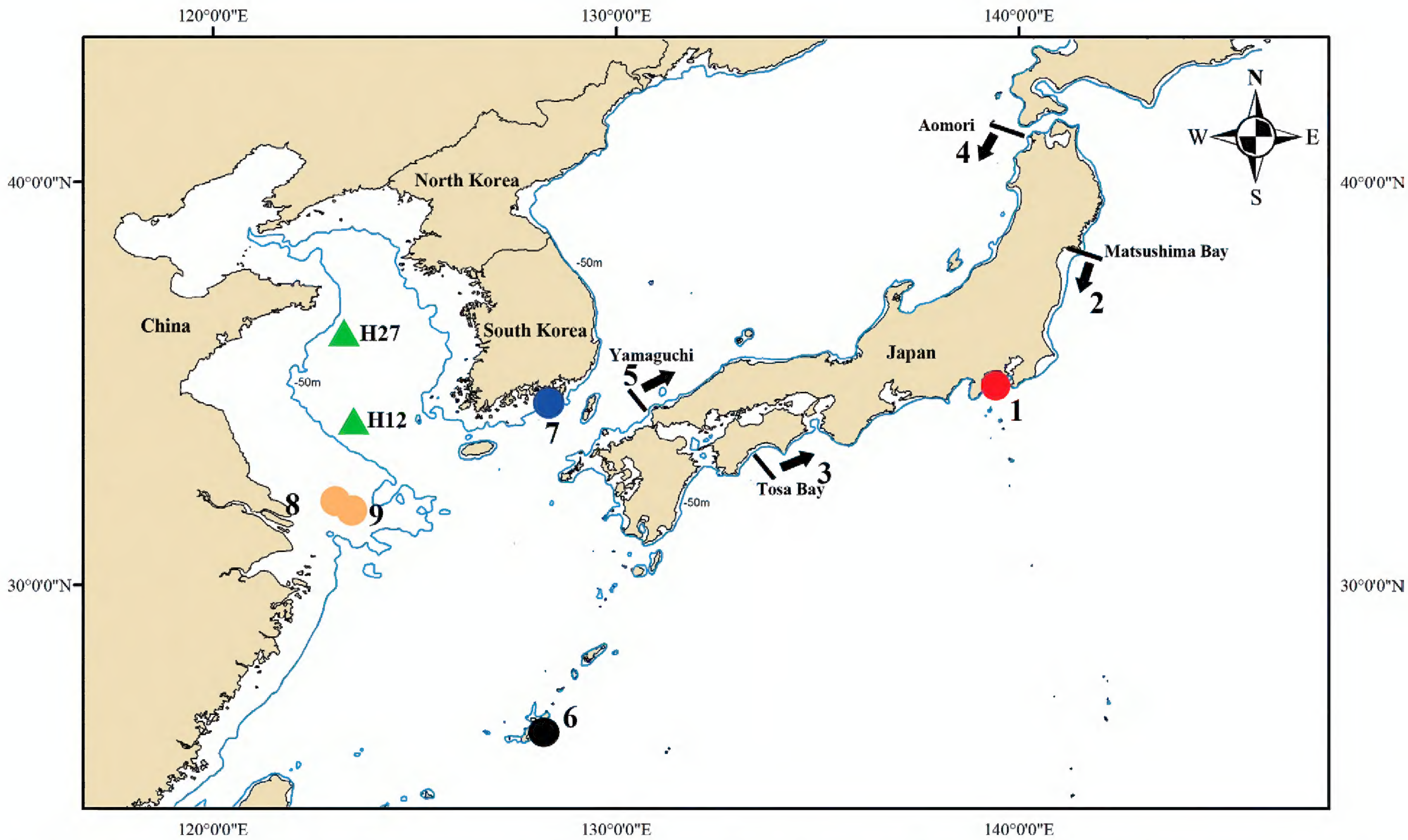

Figure 1. Historical distributional records of *S. fundicola* and the sampling stations. The red full circle 1 indicates the type locality: Sagami Bay (Jordan and Snyder 1901); black arrows 2 and 3 indicate the distribution from Matsushima Bay to Tosa Bay, and black arrows 4 and 5 indicate the distribution from Aomori Prefecture to Yamaguchi Prefectural, black full circle 6 indicates Okinawa Trough (Akihito et al. 2013); blue full circle 7 indicates the records of Tongyeong of South Korea (Choi and Lee 2019); orange full circle 8 and 9 indicate the records in the East China Sea (Okiyama 2014); the green triangles H27 and H12 point to the locations of the survey stations where the four goby specimens were caught.

Materials and methods

Specimen sampling and preservation

The fisheries resources survey vessel Lanhai 101 carried out two R/V cruises conducted by the Yellow Sea Fisheries Research Institute (YSFRI) in spring (April) and summer (July) 2022. A small Agassiz trawl (with a mouth of 1.8 m in width and 0.6 m in height) was employed during each cruise, at an average speed of 3 n mile/h (=5556 m/h) for 20 minutes. Four specimens of *S. fundicola* were collected, two in the spring (at H27 on 15 April) and two in the summer (one at H12 on 16 July and one at H12 on 20 July). The environmental parameters were obtained by the CTD measurements (SBE 911). Immediately after the capture of these specimens, the digital photographs were taken for each of them in a special glass tank with a Canon 5DSR, equipped with a micro lens (Canon), see Fig. 2. The muscle of the right lateral body was removed and stored in 95% ethanol for further molecular analysis. The voucher specimens were then fixed in 10% formalin preservative and then transformed to 75% alcohol for morphological examination and permanent curation, and deposited in the National Marine Fishery Biological Germplasm Resource Bank, China.

Morphological analysis

Meristic counts and morphometric measurements followed the methods used by Choi and Lee (2019). Additionally, two other counts (Pelvic fin rays and Dorsal fin pterygiophore formula) and one morphometric measurement (Caudal peduncle length) were used. Thus, ten meristic and twenty-one morphometric measurements were taken for each individual in this study (Table 1). Measurements and counts were taken on the left side of the specimens whenever possible. Measurements were made point

Table 1. Comparison of meristic and morphometric data of *S. fundicola* with the literature values. The numbers in bold point to the observed differences. Dorsal-fin pterygiophore formula is expressed as "3/I II II I I I 0 i/12", where "3" shows the number of vertebrae before the 1st dorsal fin is inserted, the Roman numerals in uppercase show the number of the dorsal pterygiophores inserted between the neural spines, the Roman numeral in lowercase shows the number of the interdorsal pterygiophores, and "12" shows that the two pterygiophore of the 1st ray of the second dorsal fin are mounted over the 12th vertebrae (Akihito et al. 1984; Shibukawa and Iwata 2013).

Characteristic	Present study		Original description		Choi and Lee (2019)	
	Range	Mean	Range	Mean	Range	Mean
Standard length (mm)	51.8–63.5	58.7	50.0–63.0	55.3	44.3–51.8	
Meristic counts						
First dorsal fin rays	VIII	VIII	VIII	VIII	VIII	VIII
Second dorsal fin rays	I, 16	I, 16	17–19	17.8	I, 16–17	
Anal fin rays	I, 15–16	I, 15.8	16–18	17	I, 15–16	
Pectoral fin rays	20–21	20.3			20–22	
Pelvic fin rays	I–5	I–5				
Lateral line scales	39–41	40	38–44	40.5	37–42	
Transverse scales	8–10	9.0			10–11	
Predorsal scales	10–11	10.8	10–12	10.7	8–11	
Vertebral number	14+21	14+21			14+21–22	
Dorsal-fin pterygiophore formula	3/I □ □ I I I 0 i/12					
Morphometric data						
Percentage against SL (%)						
Head length	24.5–28.0	26.1	26.0–27.0	26.3	25.9–29.7	27.8
Head depth	13.1–17.6	15.4			14.6–17.6	16.1
Head width	13.2–14.2	13.6			15.1–18.3	16.8
Snout length	4.5–5.7	5.5	5.0–7.0	6.0	5.4–7.8	6.4
Eye diameter	8.1–9.7	8.7	9.5–11.0	10.1	9.2–11.4	10.0
Interorbital width	0.9–1.9	1.4	1.0	1.0	0.7–2.1	1.5
Jaw length	8.3–10.3	9.0	10.0–11.0	10.3	8.6–11.9	10.5
Body width	10.6–10.3	11.8			10.9–14.7	12.6
Body depth at origin of first dorsal fin	15.3–22.4	18.9			15.3–19.0	16.9
Body depth at origin of anal fin	16.0–18.3	16.9			12.1–15.1	13.4
Snout to origin of first dorsal fin	31.5–33.4	32.5	32.0–36.0	33.5	28.6–36.0	33.4
Snout to origin of second dorsal fin	53.3–58.7	55.1	52.0–54.0	52.5	51.4–55.7	53.7
Snout to origin of anal fin	55.7–61.1	59.1	56.0–58.0	57.5	53.0–58.6	55.9
Caudal peduncle length	10.7–13.5	11.7	10.0–14.0	11.8		
Caudal peduncle depth	6.9–8.8	8.0	7.0–7.5	7.1	6.7–9.1	8.2
Pectoral fin length	19.5–21.8	20.6	21	21	17.7–20.9	19.0
Base of dorsal fin	13.8–14.7	14.3			13.4–16.3	14.7
Base of second dorsal fin	33.7–36.6	35.4			30.8–38.3	35.6
Base of anal fin	30.2–37.7	32.4			30.6–37.0	32.4
Caudal fin length	19.8 –23.3	21.4			18.6–27.2	22.3

to point with a digital caliper linked directly to a data-recording computer and the data were recorded to the nearest 0.1 mm. The measurements of the body were given as percentages (%) of the standard length (SL). Detailed information about the meristic and morphometric measurements is provided in Table 1. Osteological features were observed with the help of micro-CT radiographs (Bruker, skyskan-1276) or from X-rays (Aolong, version 90). Cephalic sensory canals and papillae were recorded from specimens stained with cyanine blue following Akihito et al. (1984), the notations following Sanzo (1911); Shibukawa and Aizawa (2013); Shibukawa and Iwata (2013).

DNA extraction, amplification and sequencing

DNA was extracted by using TIANamp Genomic DNA Kit (Tiangen Biotech, Beijing) according to the manufacturer's recommended protocol, and the quality was estimated at wave-length 260/280 nm by a Nano-300 micro-spectrophotometer (Allsheng, Hangzhou, China). The obtained DNA solutions were stored at -20 °C until used.

The mitochondrial *12S* rRNA (*12S*) and the *cytochrome c oxidase I* (*COI*) genes were amplified by PCR with different primer combinations. For *12S*, we used MiFish-U-F and MiFish-U-R designed by Miya et al. (2015). Primers reported by Ward et al. (2005) were used for the amplification of *COI*. PCR was conducted in 25 µl volumes, including 12.5 µl Master mix Taq, 1 µl of each primer, 1 µl template DNA, adding double distilled water to adjust the volume. Thermocycling conditions were as follows: initial denaturation for 4 min at 94 °C, denaturation for 50 s at 94 °C, annealing for 50 s at 55 °C for *COI* and 59 °C for *12S*, and extension 1 min for *COI* and 30 s for *12S* at 72 °C. After 35 cycles, the final extension was done at 72 °C for 10 min. The PCR products were bidirectional sequenced by BGI Genomics Co., Ltd.. In this study, four specimens of *S. fundicola* and three specimens of *Amblychaeturichthys hexanema* (Bleeker, 1853) were sequenced for phylogenetic analysis, and all amplified *COI* and *12S* sequences were submitted to GenBank (for the accession numbers, see Table 2).

Molecular sequence analysis

All amplified sequences of the two mtDNA genes were concatenated and used for molecular phylogenetic analysis, along with 37 GenBank-retrieved sequences from 19 related species of 14 genera belonging to the *Acanthogobius*-lineage. In addition, *Odontobutis haifengensis* Chen, 1985 (Odontobutidae) was used as an outgroup (Table 3). Multiple alignments were prepared for *COI* and *12S* sequences using the program MUSCLE in MEGA X (Edgar

Table 2. The detailed information of specimens analyzed in this study.

Species	Specimen catalog	GenBank no.		Sampling location	Resource
		COI	*12S* rRNA		
Suruga fundicola 1	YSFRI27216	OP824753	OP837791	Yellow Sea station H27	Present study
S. fundicola 2	YSFRI27217	OP824754	OP837792	Yellow Sea station H27	Present study
S. fundicola 3	YSFRI36942	OP824752	OP837789	Yellow Sea station H12	Present study
S. fundicola 4	YSFRI36943	OP824755	OP837790	Yellow Sea station H27	Present study
S. fundicola 5	CBM:ZF:15688	/	LC069781	Japan: off west of Jogashima Island	GenBank
Amblychaeturichthys hexanema 1	YSFR27208	OP824756	OP837786	North Yellow Sea	Present study
Am. hexanema 2	YSFR27209	OP824757	OP837787	North Yellow Sea	Present study
Am. hexanema 3	YSFR27210	OP824758	OP837788	North Yellow Sea	Present study
Am. hexanema 4	Uncatalogued	KT781104	KT781104	China: Qingdao, Shandong Prov.	GenBank
Acanthogobius flavimanus	Uncatalogued	MW271007	MW271007	Uncatalogued (Maybe from China)	GenBank
Ac. hasta	Uncatalogued	MK253669	MK253669	China: Lianyungang City, Jiangsu Prov.	GenBank
Chaeturichthys stigmatias	Uncatalogued	MN038166	MN038166	China: Qingdao, Shandong Prov.	GenBank
Lophiogobius ocellicauda	Uncatalogued	KR815520	KR815520	China: Zhoushan, Zhejiang Prov.	GenBank
Lepidogobius lepidus	UW:151092	KF918879	LC092050	USA: Washington, Puget Sound	GenBank
Chaenogobius gulosus	JM120726-11	KP696748	KP696748	Korea: coastal area of Jangmok	GenBank
Chaenogobius annularis	Uncatalogued	OM830225	OM830225	China	GenBank
Gymnogobius urotaenia	Uncatalogued	KT601093	KT601093	Uncatalogued (Maybe from South Korea)	GenBank
Parachaeturichthys polynema	ECSFRI-NMW01	OK012405	OK012405	China: East China Sea	GenBank
Eucyclogobius newberryi	LodgeLab Enewberryi_1	KP013101	KP013101	Uncatalogued	GenBank
Gillichthys mirabilis	Uncatalogued	FJ211845	FJ211845	China: Nantong city, Jiangsu Prov.	GenBank
Gymnogobius petschiliensis	20131115NA05	AY525784	AY525784	China: Qingdao, Shandong Prov.	GenBank
Luciogobius platycephalus	Uncatalogued	JX971538	JX971538	China: Zhoushan, Jiangsu Prov.	GenBank
L. pallidus	Uncatalogued	KF040451	KF040451	South Korea: Jeju Island	GenBank
Tridentiger bifasciatus	Uncatalogued	JN244650	JN244650	China: Zhoushan fishing ground Zhejiang Prov.	GenBank
T. trigonocephalus	Uncatalogued	KT282115	KT282115	Uncatalogued (Maybe from China)	GenBank
Rhinogobius similis	Uncatalogued	KF371534	KF371534	China: Liangzi Lake in the middle reaches of the Yangtze River	GenBank
Odontobutis haifengensis (Odontobutidae)	Uncatalogued	MF383619	MF383619	China: Fengshun, Guanggong	GenBank

Table 3. The depth (D), temperature (T), and salinity (S) of H12 and H27.

Data	Station	Bottom layer			Surface layer		
		D (m)	T (°C)	S(‰)	D (m)	T (°C)	S(‰)
April 18, 2022	H12	69.0	10.5	33.0	3.2	12.1	32.6
April 15, 2022	H27	74.0	9.5	32.8	2.8	10.5	32.6
July 16, 2022	H12	69.0	10.8	33.1	2.0	26.9	30.8
July 20, 2022	H27	74.0	9.2	32.8	2.8	25.6	30.8

2004). Genes were concatenated with the help of SequenceMatrix 1.8 (Vaidya et al. 2011). The genetic distance was calculated in MEGA X, based on Kimura 2-parameter (K2P) (Kimura 1980), and the base composition was calculated with the same software, based on K2P (Sudhir et al. 2018). The optimal evolution model was GTR selected in MEGA X based on Akaike's information criterion (AIC), and the maximum likelihood tree (ML tree) was constructed with the same software (Kumar et al. 2018), with 1,000 bootstrap replications.

Results

Suruga fundicola Jordan & Snyder, 1901

Figs 2, 3, Table 1

Suruga fundicola Jordan & Snyder, 1901: 96, fig. 20 (original description, type locality: Sagami Sea, Japan); Akihito et al. 1984: 279 (in English), fig. 253-H; Akihito et al. 2002: 1207 (in Japanese); Akihito et al. 2013: 58 (in Japanese); Shibukawa and Iwata 2013a: 45; Matsui et al. 2014: 6; Choi and Lee 2019:255, fig. 1.

Diagnosis. Distinct from all other gobies (Gobiidae), members of the *Acanthogobius*-group share a unique dominant pattern of the dorsal-pterygiophore formula, 3/I II II I I I 0 (Akihito et al. 1984). In the *Acanthogobius*-group, *S. fundicola* can be distinguished from the species of *Sagamia*, *Siphonogobius* and *Pterogobius* by possessing no free rays in the upper part of the pectoral fin and the posterior margin of the pelvic frenum indented. *S. fundicola* can be distinguished from the species of *Lophiogobius*, *Amblychaeturichthys*, and *Chaeturichthys* by the lack of barbels or flaps on the ventral surface of the head (except for the mental frenum). From species of *Acanthogobius*, *S. fundicola* can be distinguished by the large eye, its diameter greater than the snout length (vs. usually less); each cephalic sensory papilla formed into a minute skin flap (vs. not), the posterior oculoscapular canal absent (vs. posterior oculoscapular canal and its terminal pores K' and L' present).

Description of Yellow Sea specimens. The counts and measurements are given in Table 1. Dorsal-fin rays VIII-I, 16; anal-fin rays I, 15 (1), I, 16 (3); pectoral-fin rays 20 (3), 21 (1); pelvic fin rays I, 5 (4); longitudinal scales 39 (1), 40 (2), 41 (1); pre-dorsal mid-line scales 10 (1), 11 (3); transverse scales 8 (1), 9 (2); 10 (1); vertebral count 14+21 = 35 (4); dorsal-pterygiophore formula 3/I II II I I I 0 i/12; epural 2; anal-fin pterygiophores anterior to first haemal spine 2.

The following measurements are in % SL: head length 24.5–28.0 (mean 26.1); head depth 13.1–17.6 (15.4); head width 13.2–14.2 (13.6); snout length 4.5–5.7 (5.5); eye diameter 8.1–9.7 (8.7); interorbital width 0.9–1.9 (1.4); jaw length 8.3–10.3 (9.0); body width 10.6–10.3 (11.8); body depth at origin of first dorsal fin 15.3–22.4 (18.9); body depth at origin of anal fin 16.0–18.3 (16.9); snout to origin of first dorsal fin 31.5 –33.4 (32.5); snout to origin of second dorsal fin 53.3–58.7 (55.1); snout to origin of anal fin 55.7–61.1 (59.1); caudal peduncle length 10.7–13.5 (11.7); caudal peduncle depth 6.9–8.8 (8.0); pectoral fin length 19.5–21.8 (20.6); base of dorsal fin 13.8–14.7 (14.3); base of second dorsal fin 33.7–36.6 (35.4); base of anal fin 30.2–37.7 (32.4); caudal fin length 19.8–23.3 (21.4).

General body appearance was shown in Figs 2, 3. Body small, moderately elongated; predorsal body profile slightly convex; ventral profile slightly concave, especially from pectoral-fin insertion to anal-fin origin. Head large, not depressed, short but longer than wide, depth and width less than those of the body. Snout short, obtuse in lateral and dorsal view, shorter than eye diameter and postorbital head length. Eyes notably large, situated dorsolateral in upper half of the head, with very narrow interorbital space, eyes nearly meeting, diameter larger than interorbital space or snout length. Mouth almost terminal, but upper jaw slightly protruding. Maxillary concealed except at its posterior end. Tongue thick, rather broad, round anteriorly. Gill openings broad, extending anteriorly to the vertical line of the posterior margin of the eye; upper edge of the gill opening on fleshy pectoral-fin base, slightly above the upper margin. No barbels. Body covered with cycloid scales, anterior small, posterior large and the scales are rather loosely attached. Head naked.

Fins flexible, without spinous rays. First dorsal fin with 8 slender spines, reaching origin of second dorsal when depressed; dorsal-pterygiophore formula 3/I II II I I I 0 i/12. Second dorsal fin with 1 simple and 16 branched rays, shorter than the first spines. Origin of first dorsal fin posterior to a vertical through base of pectoral fins, first dorsal fin without filamentous spines. The distal margin of the first dorsal fin is convex, when adpressed, the distal tip touches the base of the spine of the second dorsal fin. Dorsal fins discontinuous. Origin of second dorsal fin somewhat at vertical through the anus, and anterior to the anal fin. When adpressed, the distal tips of the second dorsal fin and the anal fins do not reach the procurrent rays of the caudal fin. Pectoral fins rounded, with 20 rays. The pectoral fin extends posteriorly to the vertical line through the posterior margin of the base of the first dorsal fin. Pelvic fin fused into a disc, each with 1 simple and 5 branched rays. Anal fin with 15–16 rays, the anterior of the anal fin below the third branched dorsal ray of the second dorsal fin. Segmented caudal-fin rays 7+7, upper unsegmented caudal fin rays about 12 and lower unsegmented caudal fin rays about 11.

Figure 2. Lateral view of *S. fundicola*: YSFRI27216, 63.5 mm SL, photographed alive immediately upon capture.

Figure 3. Lateral (**a**), dorsal (**b**), and ventral (**c**) views of *S. fundicola*: YSFRI27216, 63.5 mm SL.

Cephalic canals are variably developed and are shown in Fig. 4: anterior oculoscapular canal (AOC) with B′, D (S), F, H'; posterior oculoscapular canal (POC) absent; preopercular canal (PC) with pores M′ and O'; four short longitudinal sensory papillae (SSP) rows (=rows r, u, s, t) on snout; four SSP rows (=rows g, j, k, and l) close behind the eye; two SSP rows (=rows h, i) before dorsal fin; two transverse sensory papillae (TSP) rows (=rows n and o) on snout and behind the eye, respectively; four longitudinal sensory papillae (LSP) rows (=rows a, b, c, and d) on the cheek; anterior end of row a approaches the anterior margin of the eye; rows b and c very close together;

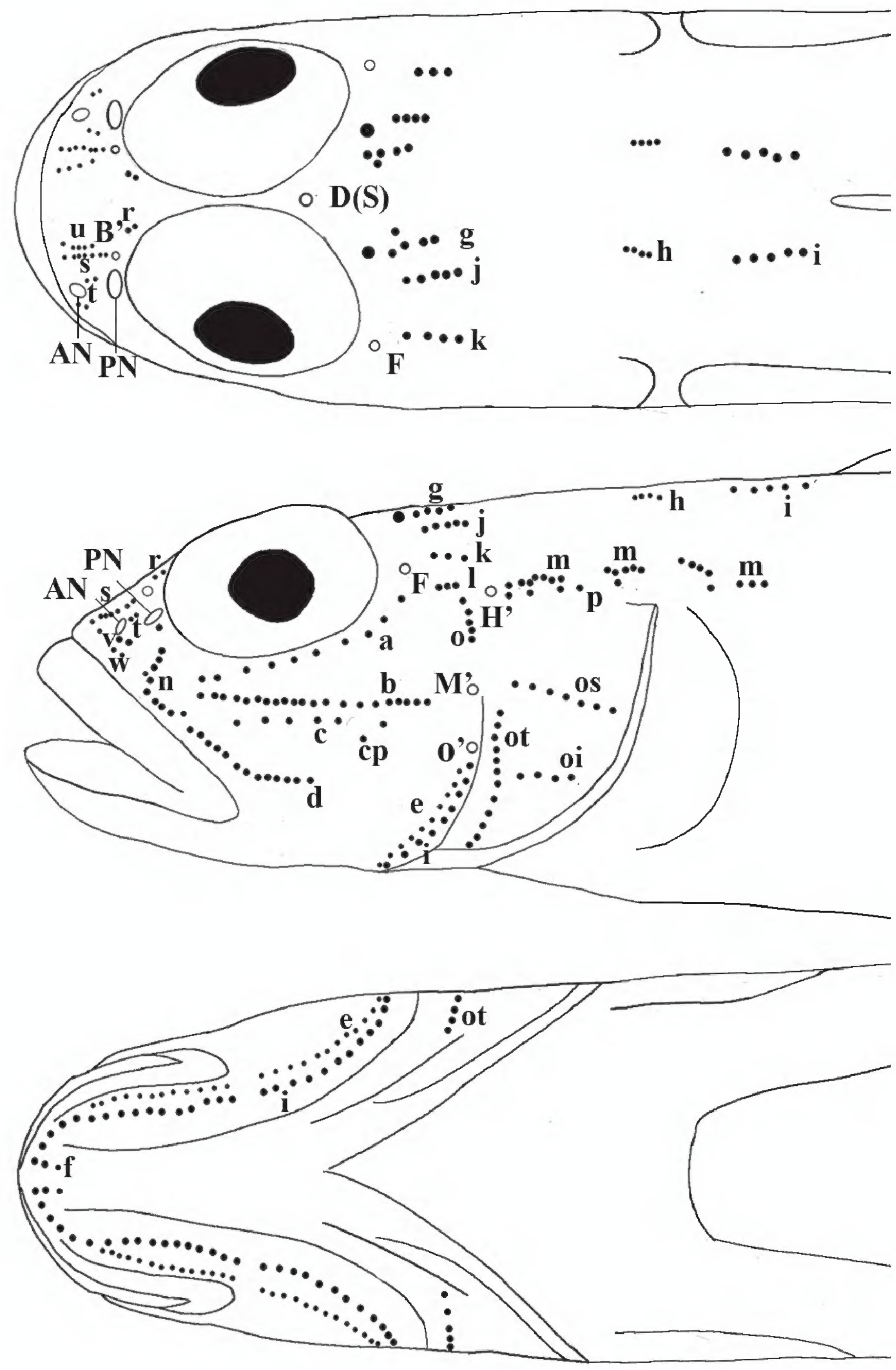

Figure 4. Dorsal (top), lateral (middle), and ventral (bottom) views of the head of *S. fundicola*: YSFRI27216, 63.5 mm SL female), showing cephalic sensory canal pores (indicated by roman uppercase letters, except for AN and PN) and papillae (indicated by roman lowercase letters). AN and PN, indicated anterior and posterior nares, respectively.

row cp with a single sensory papilla; row d arc-shaped, extending posteriorly to the vertical line through the posterior margin of the pupil; two long parallel longitudinal rows of sensory papillae just behind the chin (=row f), and ending on both sides at the opercles, one TSP row (=row ot) and two LSP rows (=rows os and oi) on the opercles, row ot extends to the ventral side.

Cranium flat, frontals extremely narrow (Fig. 5a, e). No suborbital bone. Five branchiostegal rays, the first one thin, and last one strong (Fig. 5f). Four pairs of ceratobranchials (Fig. 5g). Well-developed teeth on upper and lower pharyngeal. Three pairs of otoliths, sagittae, lapillus and asteriscus (Fig. 5e). Vertebral count 35, 14 abdominal vertebrae (av) and 21 caudal vertebrae (cv), 14 pairs of ribs appending on parapophysis (Fig. 5a, b). Three hypurals (HY), respectively HY1+2 (HY1 and HY2 fused into one), HY3+4 (HY3 and HY4 fused into one), and HY5; two epurals, EP1 and EP2.

Coloration. In freshly collected specimens (Fig. 2), head and dorsum of body dusky, darker on snout, with several irregular light-yellow blotches on the lateral body, ventral body lighter, abdomen almost white. Pupil of the eye black, iris golden gray. A light sapphirine blotch present on the gill cover. Six or seven large dark spots scattered along middle of the side from the gill opening to the caudal-fin base; 2 or 3 light orange stripes on gray dorsal and caudal fins, the anterior margin of first dorsal fin with dusky spots, the upper posterior of caudal fin with a black stripe, anal fin somewhat gray.

Coloration changed after 2 months of preservation (10% formalin preservative and then transformed to 75% alcohol), the yellow and orange pigment disappeared from body and fins, and the body of the fish became dark-yellowish, covered with tiny black spots, back darker and belly lighter, snout black, lateral dark spots not clear. Pupil of the eye white, iris golden black. Dorsal, pectoral, pelvic and anal fins light greyish.

Distribution. Northwest Pacific: off Pacific coasts from Miyagi Prefecture to Tosa Bay, Japan Sea from Aomori to Yamaguchi Prefecture, Okinawa Trough (Akihito et al. 2013), Southern Sea of Korea (Choi and Lee 2019), East China Sea (Okiyama 2014) and Yellow Sea (present study).

Habitat and ecology. The four specimens were collected at depths between 69 and 74 meters (Fig. 1). The two stations maintained a relatively low temperature of about 10 °C and a high salinity of about 33‰ in April and July 2022 (Table 3). This species is considered as one of the deepest dwelling goby in Japan, known from depths of 40 to 400 meters (Akihito et al. 2013; Choi and Lee 2019).

The catch at the stations mainly consists of ophiuroids, molluscs, jellyfishes, fishes and so on, most common species of which are the brittle stars *Ophiura sarsii vadicola* Djakonov, 1954 (Ophiuroidea) and *Stegophiura sladeni* (Duncan, 1879) (Ophiuroidea) (Fig. 6). Examples of the co-existing fish species are *Jaydia lineata* (Temminck & Schlegel, 1843) (Apogonidae), *Cleisthenes pinetorum* Jordan & Starks, 1904 (Pleuronectidae), *Liparis tanakae* (Gilbert & Burke, 1912) (Liparidae), *Pholis fangi* (Wang & Wang, 1935) (Pholidae), and *Hexagrammos otakii* Jordan & Starks, 1895 (Hexagrammidae).

Sequence characteristics and phylogenetic placement. The concatenated *COI* and *12S* sequences from 22 species were 704 bp in length (after trimming, except LC069781), including 400 conserved sites, 307 variable sites, 278 parsimony informative sites, and 24 singleton sites. The mean four nucleotide frequency of *S. fundicola* was A=26.1%, T=28.8%, C=27.3% and G=17.8%, slightly A-T rich (54.9%). The intragroup sequence divergence of *S. fundicola* was 0.5%; the genetic distance between samples of the Yellow Sea and the sequence (LC069781) of *S. fundicola* from west of Jogashima Island of Japan was 0.2%. This species has a genetic distance of 19.2% (*C. stigmatias*) to 26.3% (*E. newberryi*) to the other 20 species we used (see Table 4). The ML tree based on the concatenated sequences is shown in Fig. 7. In the tree topology, all species from the same genus clustered in one lineage; the four sequences of *S. fundicola* clustered into a highly supported (94% bootstrap P value) lineage and

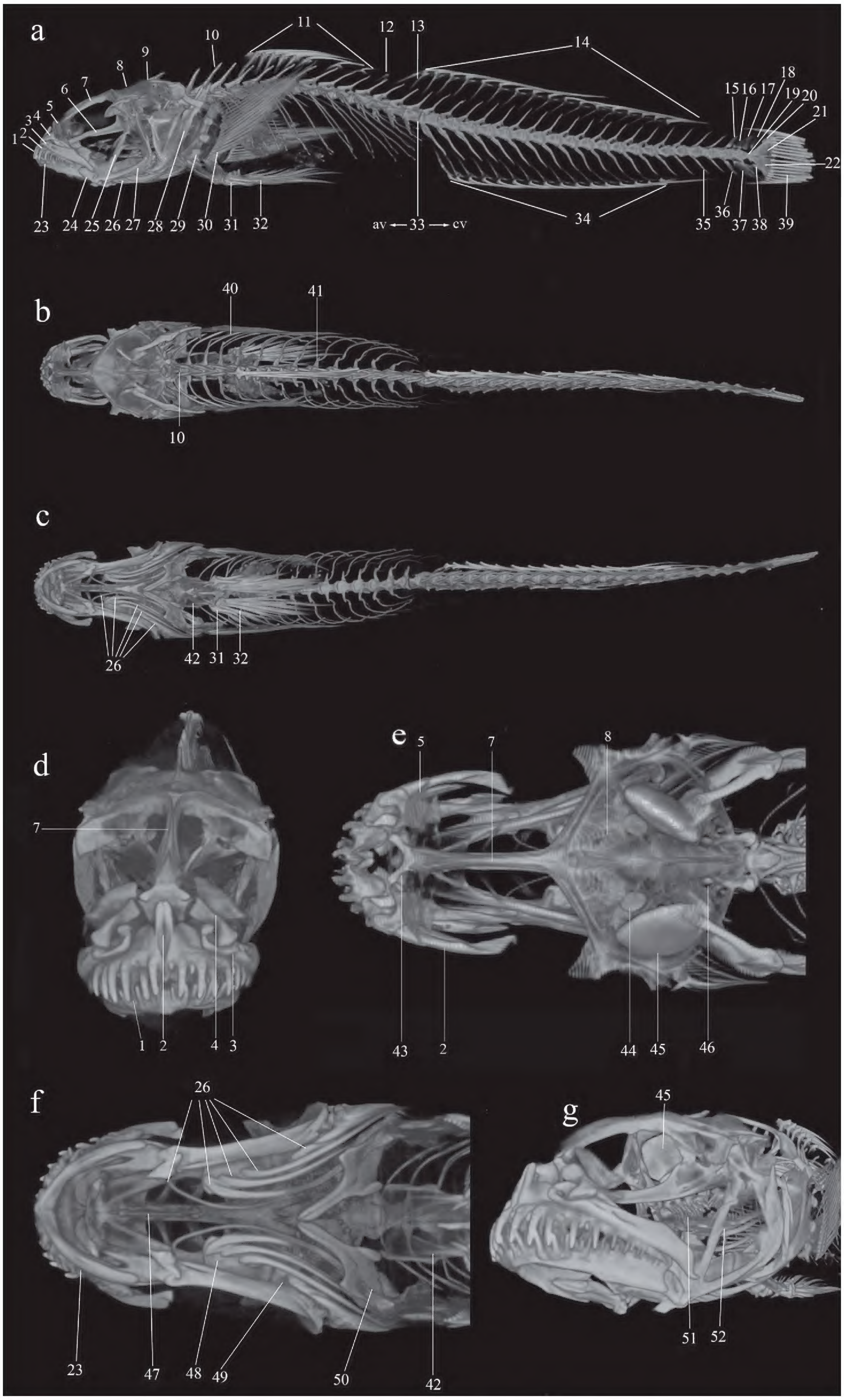

Figure 5. Micro-CT images of right (**a**), dorsal (**b**), and ventral (**c**) views of specimen YSFRI27216; front (**d**) dorsal (**e**), ventral (**f**), and oblique view (**g**) of the head of specimen YSFRI27216. 1. teeth, 2. premaxilla, 3. maxilla, 4. palatine, 5. ectethmoid, 6. parasphenoid, 7. frontal, 8. parietal, 9. supraoccipital, 10. neural spine, 11. first dorsal fin spines, 12. interdorsal pterygiophores, 13. pterygiophore, 14. second dorsal fin rays, 15. neural spine of preural centrum 3(NPU3), 16. neural spine of preural centrum 2(NPU2), 17. epural 1 (EP1), 18. epural 2 (EP2), 19. urostyle, 20. hypural 5 (HY5), 21. hypural 3+4 (HY3+4), 22. hypural 1+2 (HY1+2), 23. dental, 24. articular, 25. sympletic, 26. branchiostegal rays, 27. preopercular, 28. subopercular, 29. proximal radials, 30. pectoral fin soft rays, 31. pelvic fin spine, 32. vertebral canal, 33. boundary of abdominal vertebra and candal vertebrae, 34. anal fin rays, 35. ventrispinales, 36. haemal spine of preural centrum 3 (HPU 3), 37. haemal spine of preural centrum 2 (HPU 2), 38. parhypural (PH), 39. caudal fin ray, 40. rib, 41. parapophysis, 42. pelvic bone, 43. ethmoid, 44. lapillus 3+4 (HY3+4), 45. sagittae, 46. asteriscus, 47. basihyal, 48. ceratohyal, 3 (HPU 3). 49. epihyal, 50. cleithrum, 51. pharyngeal tooth, 52. ceratobranchial.

Figure 6. The catch of A: H27 (15 April), B: H12 (15 July), and C: H27 (20 July).

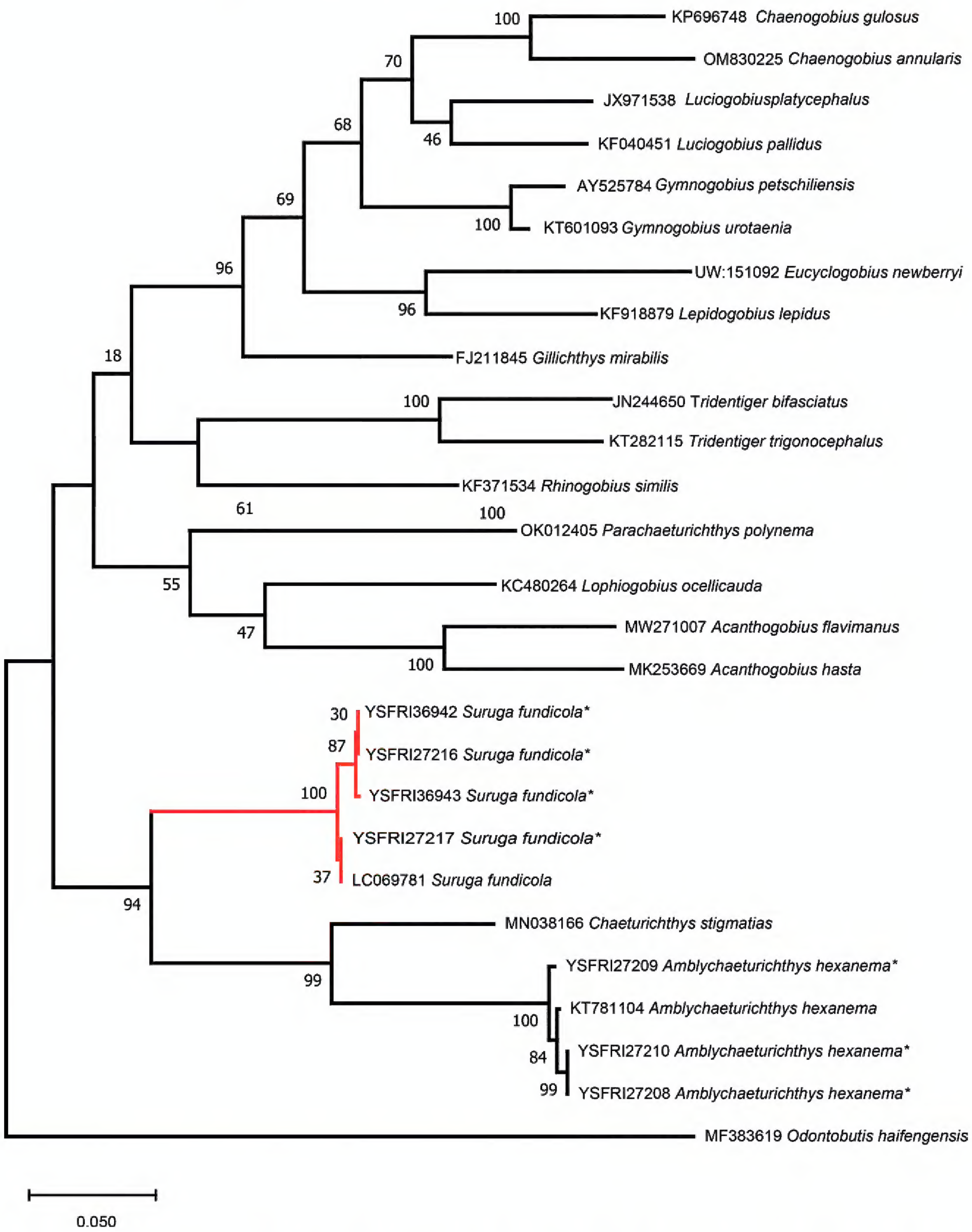

Figure 7. ML tree inferred from concatenated *COI* and *12S* sequences. Numbers at major internal nodes are bootstrap probability values. Sequences with * were sequenced in the present study.

had a sister group relationship with the lineage formed by *A. hexanema* and *C. stigmatias*.

Material examined. YSFRI27216–27217, 2 specimens, 51.2–63.5 mm SL, station H27, Yellow Sea, off Qingdao, Shandong Province, China (35°59.69'N, 123°07.63'E), collected by Changting An on 15 April, 2022; YSFRI36942, 1 specimen, 60.5 mm SL, station H12, Yellow Sea, off Lianyungang, Jiangsu Province, China (33°59.88'N, 123°24.14'E), collected by Hongyue Sun, on 16 July, 2022; YSFRI36943, 1 specimen, 59.1 mm SL, station H27, Yellow Sea, off Qingdao, Shandong Province, China (35°56.03'N 123°07.54'E), collected by Hongyue Sun, on 20 July, 2022.

Discussion

According to Jordan & Snyder's (1901) record, the type specimen (USNM 49744) was caught in a depth of 65 fathoms (119 meters), off Sagama, Japan. Unfortunately, the holotype of this species cannot be examined now, for it was lost in 1980 (Fricke et al. 2023). Our photographic

Table 4. Genetic distances (%) based on concatenated *COI* and *12S* sequences computed by MEGA X among 21 groups. *S. fundicola* * was sequenced for the present study.

	Group	Intragroup	Intergroup																			
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1.	*Suruga fundicola* *	0.5																				
2.	*S. fundicola*	n/c	0.2																			
3.	*Am. hexanema*	0.5	21.5	19.5																		
4	*Ac. flavimanus*	n/c	23.9	26.5	26.6																	
5	*Ac. hasta*	n/c	24.4	22.9	23.7	13.6																
6	*C. stigmatias*	n/c	19.2	17.9	15.1	25.6	22.8															
7	*Lo. ocellicauda*	n/c	21.6	20.1	27.3	21.2	20.9	25.5														
8	*Ch. gulosus*	n/c	23.5	14.8	26.6	24.6	25.2	23.4	20.2													
9	*Ch. annularis*	n/c	23.9	16.1	25.7	26.3	25.3	25.0	25.3	11.2												
10	*Gy. urotaenia*	n/c	21.4	18.7	25.0	24.3	22.6	23.7	23.6	15.2	15.4											
11	*Gy. petschiliensis*	n/c	23.5	22.2	25.9	26.0	23.8	25.3	24.0	16.9	16.2	2.8										
12	*P. polynema*	n/c	24.0	21.8	27.9	22.9	26.1	26.3	21.3	27.0	28.5	23.9	23.1									
13	*E. newberryi*	n/c	26.3	22.6	31.4	25.0	24.5	28.2	26.8	19.7	21.6	21.0	21.8	26.9								
14	*Gi. mirabilis*	n/c	20.9	12.6	23.9	24.7	21.4	23.3	20.6	17.4	21.4	17.1	18.7	23.4	20.1							
15	*Le. lepidus*	n/c	21.1	16.1	24.9	24.1	22.9	22.0	24.3	19.2	20.2	16.0	16.9	24.7	17.2	16.2						
16	*Lu. platycephalus*	n/c	21.4	15.5	24.5	23.2	23.8	23.6	22.2	13.7	14.0	14.1	14.8	23.3	19.3	15.6	17.5					
17	*Lu. pallidus*	n/c	22.8	20.2	22.8	23.5	22.3	21.2	24.2	15.4	15.4	13.1	14.0	24.6	19.3	15.9	16.5	10.9				
18	*T. bifasciatus*	n/c	25.0	29.0	26.2	26.3	25.4	24.7	24.5	24.4	25.1	23.2	23.5	25.0	24.4	24.7	25.3	25.1	24.6			
19	*T. trigonocephalus*	n/c	23.7	29.0	26.2	25.4	25.8	26.9	26.8	27.5	26.1	24.8	24.8	24.3	28.0	24.6	25.5	24.0	24.8	12.9		
20	*R. similis*	n/c	20.1	14.8	23.0	23.8	24.0	22.2	23.3	19.4	21.4	18.7	19.7	22.2	22.9	18.6	19.2	18.3	20.0	21.1	21.9	
21	*O. haifengensis*	n/c	22.5	23.5	27.1	24.1	26.2	26.3	24.5	25.7	26.4	22.4	21.8	24.1	24.8	24.4	22.8	22.7	20.9	29.7	27.3	22.3

examination based on two paratypes AMNH I-3549 (48.2–60.3 mm SL, Fig. 8) and their X-ray images, found that this species has notably large eyes, a very narrow interorbital space, jaws equal, eight dorsal spines and 17–18 dorsal-fin branched rays, dorsal-pterygiophore formula 3/I II II I I I 0 i /12, 17–18 anal-fin branched rays, and 35 (14 AV and 21 CV) vertebrae, as stated in its original description. All these characters are shared by the four specimens collected from the Yellow Sea of China, which are therefore conspecific with this species.

Clearly, the four specimens AMNH I-35829 (91.40–104.55 mm SL, Fig. 9), caught by Pope from Foochow (=Fuzhou), Fukien (=Fujian), China, were misidentified as they have relatively small eyes (less than the snout length), a broad interorbital space, a lower jaw projecting beyond the upper jaw, eight spines of the first dorsal fin and 16–17 branched rays of the second dorsal fin, the dorsal-fin pterygiophore formula 3/I II II I I I 0 i/11, 17–18 anal fin rays, and 34 (13 AV and 21 CV) vertebrae. Based on the number of rays in the second dorsal finI-16 (4), they can be distinguished from species of *Chaeturichthys* (I-20–22), *Siphonogobius* (I-12–13), *Pterogobius* (I-18–27), and *Acanthogobius* (I-18–20). Based on the number of anal fin rays (17–18), they are distinct from species of *Sagamia* (13–14), and *Amblychaeturichthys* (11–13). In comparison to *S. fundicola*, the eye diameter is clearly less than the snout length (vs. longer). To sum up, all the above-mentioned characters of the four specimens AMNH I-35829 are consistent with *Lophiogobius ocellicauda* Günther, 1873, as recorded by Wu and Zhong (2008).

Despite the recognition of four specimens from the Yellow Sea as *S. fundicola*, the following characteristics slightly differ from the data given in the original description. The head depth and width were less than those of the body (vs. head deeper and broader than those of the body). Based on Fig. 2, the dorsal fin has two or three light orange stripes (vs. fins dusky) and the head and dorsum of the body are dusky with several yellow markings (vs. dusky above). This body coloration is similar to that described by Shibukawa and Aonuma (2007). Nonetheless, the sampling location of the sequence (LC069781) is Kanagawa, Miura, off the west of Jogashima Island, very close to the type locality of *S. fundicola* given a 0.5% sequence divergence between this sequence and four sequences from the Yellow Sea samples, the voucher specimens of the four sequences can be recognized as the species *S. fundicola*. The aforementioned variations are probably intraspecific.

A total of 15 goby specimens from Tongyeong of South Korea were recognized as *S. fundicola* by Choi and Lee (2019). Most characteristics of the specimens are consistent with our examination of the specimens from the Yellow Sea. This study disagrees with Choi and Lee's (2019) report in two characters: head width and body depth at the anal-fin origin (Table 1). These variations can be caused by many factors, such as size-related, specimen condition, measuring method, and so on, which needs further examination. It is worth mentioning that our samples from the Yellow Sea of China (51.8–63.5 mm SL) are a bit larger than Choi and Lee's (2019) specimens of this species (44.3–51.8 mm SL).

The larval specimens, collected from two stations of the East China Sea by beam trawl in June 1956 [orange full circle 8 (32°04'N, 123°03'E) and 9 (31°53'N, 123°26'E); Fig. 1], were identified as *S. fundicola* (Okiyama 2014). We have no access to these juvenile specimens, so the possibility cannot be ruled out that they were misidentified. But, considering that the sampling locations are not far from station H12, we believe that this historical record is credible.

The species is regarded as the deepest dwelling Gobiidae in Japan, at depths from 40 to 400 meters with

Figure 8. Digital photos (**a**) and X-ray images (**b**) of the lateral body in paratypes of *S. fundicola* AMNH 3549, 48.2–60.3 mm SL, collected by D.S Honshu from Island, Japan.

Figure 9. Digital photos (**a**) and X-ray images (**b**) of the lateral body in four goby specimens AMNH 35829, 91.40–104.55 mm SL, collected by Pope from Fuzhou, Fujian Province.

a sandy silt bottom (Akihito et al. 2013; Choi and Lee 2019). The species was only discovered in two stations (H12 and H27, with a depth of about 70 m) of this survey, with a relatively low temperature of about 10 °C in summer. Moreover, many studies indicate that the Yellow Sea Cold Water Mass (YSCWM) can help the low-temperature species to escape the high temperature stress in the summer, by providing an appropriate over-summering habitat (Zhu et al. 2018; Li et al. 2021). However, up until now, there is no study indicating that *S. fundicola* is a true low-temperature species. Considering the water depth and temperature of its habitat, it is inferred that it must have some biological adaption to help it to live in this habitat. This goby species can possibly be used as an ideal experimental model for the study of adaptive evolution in a population of deep water gobies.

Suruga fundicola was assigned to the *Acanthogobius*-group based on morphological evidence (Birdsong et al. 1988; Shibukawa and Iwata 2013). But there was no molecular phylogenetic study which included a sequence of *S. fundicola*. This study also represents the first effort to address the issue about the relationship of *Suruga* within the *Acanthogobius*-lineage. The phylogenetic trees, based on concatenated *COI* and *12S* genes, indicate that *S. fundicola* has a close relationship with *A. hexanema*, and *C. stigmatias*. Based on genetic distances of the concatenated genes in our admittedly limited sampling, *S. fundicola* has the smallest genetic distances with *C. stigmatias* (19.2%). In the present study, 6 species from the *Acanthogobius*-group were clustered into two different lineages, opposite of the result of Shibukawa and Iwata (2013a). Maybe the nucleotide sequences used by us are too short and somewhat uninformative to provide a sufficient phylogenetic signal. Therefore, it is necessary to conduct more phylogenetic studies with the help of data sets based on combined nuclear and mitochondrial genes from more species to provide a more realistic insight into the phylogeny of the *Acanthogobius*-lineage (Gobiidae).

Comparative material

Suruga fundicola: AMNH I-3549, paratypes, 2 specimens, 48.2–60.3 mm SL; 1900; Suruga bay, Honshu Island, Japan (photograph examined).

Lophiogobius ocellicauda: AMNH I-35829, 4 specimens, 91.40–104.5 mm SL; Mar 1926; Foochow (=Fuzhou), Fukien (=Fujian Province), China (photograph examined).

Amblychaeturichthys hexanema: YSFRI27207–27210, 4 specimens, 60.9–85.5 mm SL; Sept 2022; Qiangdao, Shandong Province, China.

Chaeturichthys stigmatias: YSFRI 34428–34429; 12 specimens; 68.9–95.5 mm SL; Dandong, Liaoning Province, China. YSFRI 34407–34408; 2 specimens; 68.9–70.8 mm SL; Dandong, Liaoning Province, China.

Acanthogobius hasta: YSFRI 34422–34431; 10 specimens; 67.5–98.5 mm SL; Dandong, Liaoning Province, China.

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